

## Cladogram – Due next class

Where did all life come from? Most evolutionary biologists agree that all life extinct and extant came from a common ancestor. The acronym LUCA stands for Last Universal Common Ancestor.

The Bacteria are thought to be the oldest of the 3 domains (Bacteria, Archaea & Eukarya) for many reasons. One example is that they do not have introns in their DNA but eukaryotes and Archaea do. A second example is the use of Methionine as the “start” codon during protein synthesis; Bacteria use a more primitive form known as Formyl-methionine. A final example is that only one type of RNA polymerase is used in Bacteria but Archaea and eukaryotes use many different kinds.

The Archaea are thought to be older than the Eukaryotes since they do not demonstrate compartmentalization. A defining feature of Eukarya is the nucleus; all of the DNA is located inside the nucleus whereas prokaryote DNA is free in the cytoplasm.

The first group of eukaryotes was probably the Protists. Kingdom Protista has some multicellular species but are mostly unicellular. Full multicellularity did not arrive until Kingdom Plantae.

All members of Kingdom Plantae have 2 other defining features: Being autotrophic and having a life cycle known as alternation of generations. Although the Protists and prokaryotes have some autotrophic species, all plants are autotrophs that use photosynthesis to make carbon compounds.

The last 2 major Kingdoms are all heterotrophic. Once again, the Protists and prokaryote have some heterotrophic members but all Fungi and Animals are heterotrophs. Fungi are unique since they obtain their nutrients by absorption. Their food is actually digested outside of their body first and then the liquid nourishment is absorbed through their body.

On the contrary, animals ingest their food. The difference is that ingestion digests food inside of the body. Finally, a major step in the advancement of animals from all other life was the development of nerve cells.

Use the essay to fill in the data table then use the data to create a cladogram.

### A. Filling in the data table

1. Determine the **OUTGROUP**. The Outgroup is the taxon that **does not have any characters** that are present in all the other taxa. Write the name of the Outgroup in the first row as indicated.
2. Write each **taxon** in order from oldest to newest, left to right in the **first row**.
3. Write each **derived character** from oldest to newest, top to bottom in the **first column**.
4. Write a **+** in each box to show the presence of the character; do not write anything if a character is absent.

### B. Making the Cladogram

1. Draw a diagonal line with a positive slope ( / ).
2. Draw a perpendicular line from the previous line for each taxon you have. (If you have 3 taxa, draw 3 perpendicular lines off of the diagonal)
3. GOING FROM LEFT TO RIGHT: Put the **Outgroup on the first perpendicular** then the **first taxon on the second line**, etc. The "**newest**" taxon is written at the **end of the original diagonal line**.
4. For each character draw a **hash mark** to show when each character originated and write the name of the character.  
Note- Multiple characters can be in between 2 taxa.



